

## **V protein, the virulence factor across the family Paramyxoviridae: a review**

### **ABSTRACT**

Paramyxoviridae is a family of viruses within the order Mononegavirales and comprises 14 genera; Metaavulavirus, Orthoavulavirus, Paraavulavirus, Synodonvirus, Ferlavirus, Aquaparamyxovirus, Henipavirus, Morbillivirus, Respirivirus, Jeilongvirus, Narmovirus, Salemvirus, Pararubulavirus and Orthorubulavirus. The members within this family are negative and single-stranded RNA viruses including human and animal pathogens such as measles virus (MeV), Nipah virus (NiV), mumps virus (MuV), Sendai virus (SeV) and Newcastle disease virus (NDV). The V protein is conserved within the family and plays an essential role in viral pathogenicity. Although V proteins of many paramyxoviruses are interferon-antagonists which counteract with the host's innate immunity, there are still differences in the mode of action of the V protein between different genera or species within the same genera. The strategies to circumvent the host interferon (IFN) pathway can be divided into three general mechanisms; degradation of signal transducers and activators of transcription (STAT) protein, inhibition of phosphorylation of the transcription factor and, inhibition of translocation of STAT proteins into the nucleus. As a result, inhibition of IFN signalling and production promotes viral replication in the host cells. This review highlights the mechanism of the paramyxoviral V protein in evading the host IFN system.

**Keyword:** Paramyxoviridae; Mononegavirales; P gene; V protein; Interferon; Virulence factor